ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE  The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".  Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".  Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces. The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.  Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.  Sequence(s) contain n's or Xaa's which represented more than one residue. As per the rules, each nor Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (b) feature section that some may be missing.  Patentin ver. 2.0 "bug"  A "bug" in Patentin version 2.0 has caused the <220><223> section to be missing from amino acid sequence(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220><223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220><223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220><223> section for Artificial or Unknown sequences.  Skipped Sequences  Sk	ERROR DETECT	ED SUGGESTED CORRECTION SERIAL NUMBER: 09/672 7
This may occur if your file was retrieved in a word processor after creating it.  Please adjust your right margin to .3, as this will prevent "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".  The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".  The rules require that a line not exceed 72 characters in length. This includes spaces.  The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.  Non-ASCII  This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.  Sequence(s) contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.  Patentin ver. 2.0 "bug"  A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)	ATTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS WHITH MEDE INTEGRATION
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Wrapped Aminos  The amino acid number/lext at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".  Incorrect Line Length  The rules require that a line not exceed 72 characters in length. This includes spaces.  The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.  Non-ASCII  This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.  Variable Length  Sequence(s) contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.  Patentin ver. 2.0 "bug"  A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) Normally. Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. Please manually copy the relevant <220>-<223> sections for Artificial or Unknown sequences.  Skipped Sequences  Sequence(s) missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS:(I) sequence is intentionally skipped  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).		This may occur if your file was retrieved in a word processor after creating it
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(OLD RULES)  (2) INFORMATION FOR SEQ ID NO:X:  (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTI (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  This sequence is intentionally skipped  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	Skipped Sequences	Sequence(s) missing if intentional places use the following format (
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Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	•	
This sequence is intentionally skipped  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).		(xi) SEQUENCE DESCRIPTION: SEO ID NO: Y:
		This sequence is intentionally skipped
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s)
	Skinned Sequences	•
		sequence(s) missing. If intentional, please use the following format for each skipped sequence.
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<400> sequence id number		
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Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.	_ <del></del>	Use of n's and/or Xaa's have been detected in the Sequence Listing
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In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	•	In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
Use of <213>Organism Sequence(s) are missing this mandatory field or its response.	Use of <213>Organism	
(NEW RULES)	(NEW RULES)	are missing this mandatory field or its response.
Use of <220>Feature Sequence(s)	Honor 2000 F	
are missing the <220>Feature and associated headings	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES)  Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"	(MEAN MOLES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"

(Sec. 1.823 of new Rules)

Please explain source of genetic material in <220> to <223> section.

(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)

11

12

\_\_ Patentin ver. 2.0 "bug"

OIPE

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/672,725

DATE: 10/06/2000
TIME: 12:46:04
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Output Set: N:\CRF3\10062000\1672725.raw

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4 <110> APPLICANT: Stocker, Penny J.

5 Steimel-Crespi, Dorothy T.

6 Crespi, Charles L.

7 Rief, Timothy C

8 Patten, Christopher J.

10 <120> TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF

13 <130> FILE REFERENCE: G0307/7017

C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/672,725

C--> 15 <141> CURRENT FILING DATE: 2000-09-28

15 <150> PRIOR APPLICATION NUMBER: US 60/156,510

16 <151> PRIOR FILING DATE: 1999-09-28

18 <160> NUMBER OF SEQ ID NOS: 32

20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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## ERRORED SEQUENCES

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24 <212> TYPE: DNA
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31 <400> SEQUENCE: 1
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Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys
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Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
40
       30
                                        35
                                                                        40
     tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile 45 50 55 60
                                                                                                                 196
45
     cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr 65 70 75
                                                                                                                244
     gat agc ttt.gca aat gca gga att tca aga aac aaa act ttt cca gtt Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
                                                                                                                292
                        80
                                                      85
     ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His 95 100 105
     ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt
```

RAW SEQUENCE LISTING DATE: 10/06/2000 PATENT APPLICATION: US/09/672,725 TIME: 12:46:04

					000					1200	0200	0 (20	, , , ,	J.14	••			
	61 62		110	Glu				115			-	-	120		-		-	
	64 65	Ala	ggc Gly	gtg Val	ctg Leu	gtg Val	Ala	gct Ala	tac Tyr	atc Ile	cag Gln	gtt Val	tca Ser	ttc Phe	tgg Trp	tgc Cys	ctg Leu	436
	66	125					130					135					140	
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	69 70			Gly		145					150					155		
	72	atc	atg	cga	cag	gag	att	ggc	tgg	ttt	gac	gtg	cat	gac	gtt	ggg	gag	532
	73 74			Arg	160					165					170			
	76	ctt	aac	acc	cgg	ctc	aca	gac	gat	gtc	tcc	aaa	atc	aat	gaa	gga	att	580
	77 78			Thr 175					180					185				
	80	ggc	gac	aaa	att	gga	atg	ttc	ttt	cac	tça	ata	gca	aca	ttt	ttc	acc	628
	81 82	Gly	Asp 190	Lys	Ile	Gly	Met	Phe 195	Phe	His	Ser	Ile	Ala 200	Thr	Phe	Phe	Thr	
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	85	Gly	Phe	Ile	Val	Gly	Phe	Thr	Arg	Gly	Trp	Lys	Leu	Thr	Leu	Val	Ile	
	86	205					210		•	_	_	215					220	
	88	ttg	gcc	atc	agc	cct	gtt	ctt	gga	ctt	tca	gcc	gcc	atc	tqq	qca	aag	724
	89			Ile														
	90					225					230				•	235	•	
	92			tct														772
	93	Ile	Leu	Ser	Ser	Phe	Thr	Asp	Lys	Glu	Leu	Leu	Ala	Tyr	Ala	Lys	Ala	
	94				240					245					250			
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	97 98	Gly	Ala	Va1 255	Ala	Glu	Glu	Val	Leu 260	Ala	Ala	Ile	Arg	Thr 265	Val	Ile	Ala	
	100																gaa	868
	101	Phe	Gly	gly	Glr	Lys	Lys	Glu	Leu	ı Glu	Arg	Tyr	Asr	Lys	Asn	Let	Glu	
	102 104	gaa	270 gct		. gga	att	qqq	275 rata		raaa	. act	ato	280 aco		aac	att	tct	916
-	105																Ser	
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	109																Phe	
	110					305					310	)				315	,	
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	113	Trp	Tyr	Gly	Thr	Ser	Leu	Val	Leu	Ser	Ser	Glu	Tyr	Ser	Ile	Gly	Gln	
	114				320					325					330			
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	L17	Val	Leu	Thr	Val	Phe	Phe	Ser	Val	Leu	Ile	Gly	Ala	Phe	Ser	Ile	Gly	
	118			335					340					345				
	L20	cag	gca	tcc	cca	agc	att	gaa	gca	ttt	gca	aac	gca	aga	gga	gca	gct	1108
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	L22		350					355					360					
	L24	tat	gaa	atc	ttc	aag	ata	att	gac	aat	aaa	cca	agc	att	gac	ago	tat	1156
1	125	Tyr	Glu	Ile	Phe	Lys	Ile	Ile	Asp	Asn	Lys	Pro	Ser	Ile	Asp	Ser	Tyr	

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 DATE: 10/06/2000

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126	365					370					375					380	
128								gat									1204
. 129	Ser	Lys	Ser	Gly	His	Lys	Pro	Asp	Asn	Ile	Lys	Gly	Asn	Leu	Glu	Phe	
130					385					390					395		
132	aaa	aat	gtt	cac	ttc	agt	tac	cct	tct	cga	aaa	gaa	gtt	aag	atc	tta	1252
133	Lys	Asn	Val	His	Phe	Ser	Tyr	Pro	Ser	Arg	Lys	Glu	Val	Lys	Ile	Leu	
134				400					405					410			
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137	Lys	Gly	Leu	Asn	Leu	Lys	Val	Gln	Ser	Gly	Gln	Thr	Val	Ala	Leu	Val	
138			415					420					425				
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141	Gly	Asn	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Thr	Val	Gln	Leu	Met	Gln	Arg	
142		430					435		1			440				-	
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145								Met									
146	445	-	-			450	•			4	455	•				460	
148	aqq	acc	ata	aat	gta	aqq	cat	ctt	caa	qaa	att	act	gat	ata	ata	agt.	1444
149								Leu									
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152	caq	qaq	cct	ata	tta	ttt	qcc	acc	acq	ata	act	gaa	aac	att	cgc	tat	1492
153								Thr									
154				480					485					490		- 4 -	
156	qqc	cqc	qaa	aat	qtc	acc	atq	gat	qaq	att	gag	aaa	act	att	aaσ	σaa	1540
157								Asp									
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161								Met									
162		510		-4-			515		-1-			520	-1-				
164	ctq		σσa	gag	aga	aaa	acc	cag	cta	agt.	aat		саσ	aaa	cag	aαa	1636
165								Gln									
166	525		2		5	530					535	G-1		_10	0	540	
168		acc	att	act	caa		cta	gtt	cac	aac		ааσ	att	ctt	cta		1684
169								Val									1004
170					545				3	550				Lu	555	200	•
172	gat	gag	aca	асσ		act	cta	gac	act		agt	gaa	aca	ata		cad	1732
173								Asp									1/52
174	шър	Olu	1114	560	001	2124	ncu	1150	565	UIU	UCI	Olu	nru	570	Val	GIII	
176	ata	acc	cta		ааσ	acc	aga	aaa		caa	act	acc	att		ata	act	1780
177		_	-	_		-	_	Lys								_	1700
178	• • •	2114	575	пор	цуJ	niu	A1 9	580	GLy	AI 9	1111	1111	585	Val	116	AIG	
180	cat	cat		tet	aca	att	cat	aat	acc	rat	ata	2++		aat	+++	ant.	1828
181								Asn									1020
182	nis	590	neu	261	1111	val	595	HSII	Ala	кэр	vaı	600	нта	GIY	Pile	ASP	
184	ant.		a+a	a++	a+ a	~~~		~~~	22+	aa+	a > +		ata	-+-		~~~	1076
185								gga									1876
186	605	GIY	vai	ire	val		ьys	Gly	ASII	нта	_	GIU	neu	Mer	цуS		
188		~~~	-++	+	++-	610	~++	~+~	265	a <b>+</b> -	615			~ ~ -		620	1004
189								gtc									1924
190	цγѕ	σтλ	тте	TAL		тÃ2	ьeu	Val	THE		GIN	THE	Arg	стλ		GIU	
190					625					630					635		

 RAW SEQUENCE LISTING
 DATE: 10/06/2000

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Input Set : A:\485402\_1.txt
Output Set: N:\CRF3\10062000\1672725.raw

192 att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc 193 Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg toa act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu 670 675 680 ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg
Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
685 690 695 700 agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly 705 710 715 ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile 720 725 730 ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu 750 755 760 gga att att tot ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly 765 770 aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr 800 805 810act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys ggg gct ata ggt too agg ctt gct gtc att acc cag aat ata gca aat Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn 830 835 840 ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val 865 870 875 gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Glu Leu 880 885 890 2.54 gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act  RAW SEQUENCE LISTING PATENT APPLICATION: US/09/672,725 DATE: 10/06/2000 TIME: 12:46:04

257 258	Glu	Gly	Ala 895	Gly	Lys	Ile	Ala	Thr 900	Glu	Ala	Ile		Asn 905	Phe	Arg	Thr	
260	att	att		tta	act	caa	gag		aag	+++	gaa			tat	gca	cag	2788
261									Lys								2,00
262	,	910	501	200		**** 9	915	01	2,0			920	****	-1-		0111	
264	agt		caa	αťa	cca	tac		aac	tct	tta	agg		aca	Cac	ato	ttc	2836
265									Ser								2030
266	925	пси	OLII	, ar	110	930	ni 9	4311	Jei	ne u	935	ny 5	пта	1113	110	940	
268		ato	tca	+++	tát		acc	car	gca	ato		tat	+++	too	tat		2884
269		•						-	Ala	_	_					-	2004
270 ·	GIŽ	Val	261	FIIC	945	116	1111	GIII	AIG	950	Het	TÄT	FILE	Ser	955	VIG	
272	aac	+ ~ +	tta	aaa		aat	acc	+ = 0	ttg		ac =	2 2 ±	a a a	++0		220	2932
273									Leu								2934
274	GLY	Cys	rne	960	FIIC	GIY	ALG	TYT	965	Val	мта	ASII	GIU	970	nec	ASII	
276	+++	020	an t		a++	++~	at a	++0	tca	act	2++	a+ 0	+++		aaa	2+4	2980
270 277									Ser								2300
277 278	File	GIII	975	Val	пеп	ьец	Val	980	261	мта	116	Val	985	Gry	нта	net	
280	~~~	~+~		~~~	~+~		+	:	+	+	~~~				~~~		2020
									gct								3028
281	ALd		GIY	GIN	vaı	ser		Pne	Ala	PIO			Ala	гаг	Ald	гаг	
282		990					995					1000		4		- 6 6	2076
284									atc								3076
285			Ala	ALA	HIS			met	Ile	шe			Ser	Pro	Leu		
286	1005					1010					1015					1020	
288									aag								3124
289	Asp	Ser	Tyr			His	СТУ	Leu	Lys		Asn	Thr	Leu			Asn	
290					L025				-	L030				_	1035		
292									aac								3172
293	Val	Thr			Glu	Val	Val		Asn	Tyr	Pro	Thr			Asp	Ile	
294				L040					1045					1050			
296									gag								3220
297	Pro			Gln	Gly	Leu			Glu	Val	Lys	-	_	Gln	Thr	Leu	
298			L055				_	L060				_	L065				
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302		L070					1075					1080					
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305			Arg	Phe	Tyr	-		Leu	Ala	Gly			Leu	Ile	Asp		
306	1085					1090					1095					1100	
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313	Ile	Val	Ser	Gln	Glu	Pro	Ile	Leu	Phe	Asp	Cys	Ser	Ile	Ala	Glu	Asn	
314			]	1120				1	L125				1	130			
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318		1	135				1	140				1	145				
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321	Gln	Ala	Ala	Lys	Glu	Ala	Asn	Ile	His	His	Phe	Ile	Glu	Thr	Leu	Pro	
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PATENT APPLICATION: US/09/672,725 TIME: 12:46:04 Input Set : A:\485402\_1.txt Output Set: N:\CRF3\10062000\1672725.raw 322 1150 1155 gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly 324 3556 325 326 1165 1170 1175 1180 328 ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct 3604 Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro 1185 1190 1195 329 330 cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt 3652 His Ile Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser 1200 1205 gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr 1215 1220 12253700 336 337 338 tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu 1230 1235 1240 340 341 342 ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln 3796 344 345 1245 1250 346 1255 348 cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln 1265 1270 1275 3844 349 350 gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tatttttaa 3899 Ala Gly Ala Lys Arg 353 1280 tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accaagttca qaqtcttcaq attttataat taaaggaacc aaaagaaaca ttatctgatg gaataaaata ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt gtataatttt tgtttatatt ttatttgtaa ettactgett tgetgaaaga ttatagaagt 4199 361 ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat End of line E--> 362 caaaaaaaa aaaaaaaaaa 364 <210> SEQ ID NO: 2 365 <211> LENGTH: 1281 nucleic acid number 366 <212> TYPE: PRT 367 <213> ORGANISM: Canis familiaris missing. All lines 369 <400> SEQUENCE: 2 Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn Phe Trp 371 Lys Met Glý Lys Lys Ser Lys Lys Asn Glu Lys Lys Glu Lys Lys Pro 20 25 30 must have numbering Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp Arg 40 Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala Ala 50 60 377 Computer program Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr Asp Ser Phe Ala 379 70 75 Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val Ile Ile Asn Glu only counts 4259. This causes an error

DATE: 10/06/2000

RAW SEQUENCE LISTING

between the number

listed, (ZII) 4279

and number found:

4259

**RAW SEQUENCE LISTING**PATENT APPLICATION: US/09/672,725

DATE: 10/06/2000

TIME: 12:46:04

Input Set : A:\485402\_1.txt
Output Set: N:\CRF3\10062000\1672725.raw

382 Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His Leu Glu Glu Glu 383 100 105 110 Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly Ala Gly Val Leu 115 120 125384 385 Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu Ala Ala Gly Arg 130 135 140 386 387 388 Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala Ile Met Arg Gln 150 155 Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu Leu Asn Thr Arg 165 170 175 390 Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile Gly Asp Lys Ile 180 185 190 392 Gly Met Phe Phe His Ser Ile Ala Thr Phe Phe Thr Gly Phe Ile Val 195 200 205 394 395 Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile Leu Ala Ile Ser 210 215 220 396 397 Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys Ile Leu Ser Ser 225 230 240 398 399 Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala Gly Ala Val Ala 245 250 255 400 401 Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala Phe Gly Gly Gln 260 265 270 402 403 Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys Gly 275 280 285 404 405 Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala Ala 290 295 300 407 Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Thr 305 310 315 320 409 Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln Val Leu Thr Val 325 330 335 410 411 Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly Gln Ala Ser Pro 340 345 350412 413 Ser Ile Glu Ala Phe Ala As<br/>n Ala Arg Gly Ala Ala Tyr Glu Ile Phe $355 \hspace{1.5cm} 360 \hspace{1.5cm} 365 \hspace{1.5cm}$ 414 415 Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser Gly 370 375 380416 417 His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe Lys Asn Val His 385 390 395 400 418 419 Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu Asn  $405 \hspace{1.5cm} 410 \hspace{1.5cm} 415 \hspace{1.5cm}$ 420 421 Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser Gly 420 425 430422 423 Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp Pro  $435 \hspace{1cm} 440 \hspace{1cm} 445$ 424 Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile Arg Thr Ile Asn 450 455 460 Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser Gln Glu Pro Val 465 470 475 480 428 Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu Asn

DATE: 10/06/2000 TIME: 12:46:04

431					485					490					495	
432	Val	Thr	Met	Asp	Glu	Ile	Glu	Lys	Ala	Val	Lys	Glu	Ala	Asn	Ala	Tyr
433				500					505					510		
434	Asp	Phe	Ile	Met	Lys	Leu	Pro	Asn	Lys	Phe	Asp	Thr	Leu	Val	Gly	Glu
435	-		515		-			520	-		-		525		_	
436		Glv	Ala	Gln	Leu	Ser	Glv	Glv	Gln	Lvs	Gln	Ara	lle	Ala	Ile	Ala
437		530					535	U-1		-12		540				
438			T.e.11	Val	Δνα	Δen		Lve	Tlo	T.e.u	Len		Asn	Glu	Ala	Thr
439		AIG	пси	vul	ALG	550	110	Lys	110	LCu	555	LCu	1156	O.L.	21.24	560
440		7.1.	T 011	λαν	mbr		cor	C1.	717	37 - 1		Cln	17 - 1	Ala	Len	
		Ald	Leu	ASP	565	Giu	ser	Gru	мта	570	Val	GIII	Val	AIG	575	rsb
441		.1.	3	T		7	mb as	mb so	т1.		TIO	110	II i o	7 ~~		con
442	-	Ala	Arg	-	GTA	Arg	THE	THE		Val	116	АТА	nis	Arg 590	пец	ser
443			_	580		_		- 1	585	<b>a</b> 1	n)				17- 1	T1 -
444		Val		Asn	Ala	Asp	vaı		Ата	GTĀ	Pne	Asp		Gly	Val	ire
445			595		_	•	_	600	_		_	~ 1	605	~ 1	-1.	
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777										Ala							2075
	Val	PIQ	туг	930	ASII	ser	ьец	AIG	935	AIA	nis	116	FILE	940	Val	Ser	
778							~ <del>*</del> ~	-+-		+++	+	+-+	a a t		+~+	++0	2943
780	TET	TCT	atc	acc	cag	gca	acg	atg	mar	ttt	Con	m	315	990	Cura	Dho	2343
781	Pne	ser		Thr	GIN	Ala	met		TAL	Phe	ser	TAT		GIY	Cys	Pile	
782			945		4		_, .	950			L		955	444		~~±	2001
784										gag							2991
785	Arg		GTĀ	Ala	Tyr	Leu		Ala	Asn	Glu	rne		Asn	rne	GIN	ASP	
786		960					965					970					2020
788										ttt							3039
789	Val	Leu	Leu	Val	Phe	Ser	Ala	Ile	Val	Phe	Gly	Ala	Met	Ala	۷al	GTA	

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Input Set : A:\485402\_1.txt Output Set: N:\CRF3\10062000\1672725.raw

790 975 cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa gta tca gca Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala 995 1000 1005 gcc cac gtc atc atg atc att gaa aaa agc cct ctg att gac agc tac Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile Asp Ser Tyr 1010 1015 1020 age cet cae gge etc aag eea aat aeg ttg gaa gga aat gtg aca ttt Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn Val Thr Phe 1025 1030 1035 aat gag gtc gtg ttc aac tat ccc act cga cca gac atc ccc gtg ctc Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val Leu . 1045 cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg gcc ctc gta
Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val
1055 1060 1065 1076 ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc cta gag cgc Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc aaa gag ata Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly Lys Glu Ile 1090 1095 1100 aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc atc gtg tct Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser 1105 1110 1115 cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac att gcc tat Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn Ile Ala Tyr 1120 1125 1130 1120 1125 gga gac aac agc cgg gte gta tca cat gaa gag att atg cag gcc Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met Gln Ala Ala 1135 1140 1145 1155 aag gag gcc aac ata cac cac ttc atc gag aca ctc cct gag aaa tac Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro Glu Lys Tyr 1155 1160 1165 aac acc aga gta gga gac aaa gga acc cag ctc tct ggt ggc cag aaa Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys 1170 1175 1180 cag cgc att gcc atá gct cgc gct ctt gtt aga cag cct cat att ttg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt gaa aag gtt Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc tgc att gtg Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val 1215 atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta ata gtg gtg Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val

Input Set : A:\485402\_1.txt Output Set: N:\CRF3\10062000\1672725.raw ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa cag ctg ctg Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln Gln Leu Leu 3855 857 1255 1260 1250 858 gct cag aaa ggc atc tat ttt tcc atg atc agt gtc cag gct gga gca 860 Ala Gln Lys Gly Ile Tyr Phe Ser Met Ile Ser Val Gln Ala Gly Ala 1265 1270 1275 3952 aag cgc tag tgaactgtgg ccatatgagc tgttaaatat tttttaatat Tovalid end of

4312

1 Ince numbering

refer to p. 6 ttgtgttaaa acatggcatt taatcaaagt taaaaggtga gcacttactg gaaaaactat 868 gtagaactac ctgtttaaca tttcttgctg caactgaaga tcattccacc aagttcagag tottoagatt ttataattaa aggaaccaaa agaaacatta totgatggaa taaaatattg 870 gtgttaattg cattataaaa ttatagagta attcaaagta gattttgtta ataaattgta 871 taatttttgt ttatatttta tttgtaactt actgctttgc tgaaagatta tagaagtggt 872 873 E--> 874 aaaaa 1641 <210> SEQ ID NO: 22 1642 <211> LENGTH: 4279 1643 <212> TYPE: DNA 1644 <213> ORGANISM: Canis familiaris 1646 <220> FEATURE: 1647 <221> NAME/KEY: CDS 1648 <222> LOCATION: (17)...(3859) 1650 <400> SEQUENCE: 22 1651 ggagcgcgag gtcggg atg gat cct gaa gga ggc cgt aag ggg agt gca gag Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu 1652

5

70

105

aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aat gag aag aaa

Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys Lys 15 20 25

gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn 30 35 40

tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile 45 50 55 60

cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr

gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt

Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val

ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat

Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His

ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt

Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
110 115 120

100

1683 gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg

115

65

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1656 1657

1659 1660 1661

1663 1664 1665

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1684	Ala	Gly	Val	Leu	Val	Ala	Ala	Tyr	Ile	Gln	Val	Ser	Phe	Trp	Cys	Leu	
1685	125					130					135					140	104
1687	gca	gca	gga	aga	cag	ata	ctc	aaa	att	aga	aaa	caa	ttt	ttt	cat	gct	484
1688	Ala	Ala	Gly	Arg	Gln	Ile	Leu	Lys	Ile	Arg	Lys	Gln	Phe	Phe	His	Ala	
1689					145					150		•			155		
1691	atc	atg	cga	cag	gag	att	ggc	tgg	ttt	gac	gtg	cat	gac	gtt	ggg	gag	532
1692	Ile	Met	Arg	Gln	Glu	Ile	Gly	Trp	Phe	Asp	Val	His	Asp	Val	Gly	Glu	
1693				160					165					170			
1695	ctt	aac	acc	cgg	ctc	aca	gac	gat	gtc	tcc	aaa	atc	aat	gaa	gga	att	580
1696	Leu	Asn	Thr	Arg	Leu	Thr	Asp	Asp	Val	Ser	Lys	Ile	Asn	Glu	Gly	Ile	
1697			175					180					185				
1699	qqc	qac	aaa	att	gga	atg	ttc	ttt	caa	tca	ata	gca	aca	ttt	ttc	acc	628
1700	Gly	Ásp	Lys	Ile	Gly	Met	Phe	Phe	Gln	Ser	Ile	Ala	Thr	Phe	Phe	Thr	
1701		190					195					200					
1703	ggt	ttt	ata	gtg	ggg	ttt	aca	cgt	ggt	tgg	aag	cta	acc	ctt	gtg	att	676
1704	Ğĺv	Phe	Ile	Val	Gly	Phe	Thr	Arg	Gly	Trp	Lys	Leu	Thr	Leu	Val	Ile	
1705	205					210					215					220	
1707	tta	qcc	atc	agc	cct	gtt	ctt	gga	ctt	tca	gcc	gcc	atc	tgg	gça	aag	724
1708	Leu	Ala	Ile	Sér	Pro	Val	Leu	Gly	Leu	Ser	Ala	Ala	Ile	Trp	Ala	Lys	
1709					225					230					235		
1711	ata	cta	tct	tca	ttt	act	gat	aaa	gaa	ctc	tt.g	gcc	tat	gca	aaa	gct	772
1712	Tle	Leu	Ser	ser	Phe	Thr	Asp	Lys	Glu	Leu	Leu	Ala	Tyr	Ala	Lys	Ala	
1713				240					245					250			
1715	дда	gca	αta	act	gaa	qaa	qtc	tta	gca	gca	atc	aga	act	gtg	att	gcc	820
1716	Glv	Ala	Val	Ala	Glu	Ğlu	Val	Leu	Āla	Āla	Ile	Arg	Thr	Val	Ile	Ala	
1717	017		255					260					265				
1719	+++	gga	aga	caa	aag	aaa	qaa	ctt	gaa	agg	tac	aac	aaa	aat	tta	gaa	868
1720	Phe	Glv	Glv	Gln	Lvs	Lvs	Ğlu	Leu	Ğ1u	Arg	Tyr	Asn	Lys	Asn	Leu	Glu	
1721		270					275					280					
1723	gaa	act	aaa	σσα	att	ववव	ata	aag	aaa	gct	atc	acg	gcc	aac	att	tct	916
1724	Glu	Ala	Lvs	Ğĺv	Ile	Gly	Ile	Lys	Lys	Ala	Ile	Thr	Ala	Asn	Ile	Ser	
1725	285					290					295					300	
1727	att	aat	acc	act.	ttc	tta	tta	atc	tat	gca	tca	tat	gct	ctg	gct	ttc	964
1728	Tle	Glv	Ala	Ala	Phe	Leu	Leu	Ile	Tyr	Ala	Ser	Tyr	Ala	Leu	Ala	Phe	
1729	110	011			305				-	310					315		
1731	taa	tat	aaa	acc	tec	tta	atc	ctc	tcc	agt	gaa	tat	tct	att	gga	caa	1012
1732	Trn	Tyr	Glv	Thr	Ser	Leu	Val	Leu	Ser	Ser	Glu	Tyr	Ser	Ile	Gly	Gln	
1733	TIP	+1-	027	320					325					330			
1735	αta	ctc	act	atc	ttc	ttt	tct	αta	tta	att	qqq	gct	ttt	agt	att	gga	1060
1736	Val	Leu	Thr	Val	Phe	Phe	Ser	Val	Leu	Ile	Gly	Āla	Phe	Ser	Ile	Gly	
1737	. • •	пси	335					340			-		345				
1739	can	aca	tcc	cca	aαc	att	gaa			qca	aac	gca	aga	gga	gca	gct	1108
1740	Cln	9Cα 11a	Cor	Dro	Ser	Tle	Glu	Ala	Phe	Ala	Asn	Āla	Arq	Gly	Āla	Āla	
1741	GII	350					355					360	,	-			•
1741	+ = +	220	ato	++0	aan	ata			aat	aaa	. cca	aqc	att	gac	ago	tat	1156
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1744	365		116			370					375	;		•		380	
1747	+00		a ort	aa-	cat	222	cca	αat	aat	at+			aat	tto	gaa	ttc	1204
	cor	aay	Cov	. 99ª	. uut	Tave	Pro	Asr	Asn	Ile	Lvs	Gĺv	Asn	Leu	Ğlu	Phe	
1748	sei	гуу	. ser	GIY	1113	ப்பி						1			-		

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4.5.4.0			•														
1749					385					390					395		
1751	aaa	aat	gtt	cac	ttc	agt	tac	cct	tct	cga	aaa	gaa	gtt	aag	atc	tta	1252
1752	Lys	Asn	Val		Phe	Ser	Tyr	Pro	Ser	Arg	Lys	Glu	Val	Lys	Ile	Leu	*
1753				400					405					410			
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1756	Lys	Gly	Leu	Asn	Leu	Lys	Val	Gln	Ser	Gly	Gln	Thr	Val	Ala	Leu	Val	
1757			415					420					425				
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1760									Thr								
1761	-	430		•	-	-	4.35					440				5	
1763	ctc	tat	gac	CCC	aca	gat.	aac	atα	gtc	tat	att	gat	αпа	саσ	gac	att	1396
1764									Val								1000
1765	445	-1-				450	0-1	*****	, 41	010	455	пор	013	0.111	nsp	460	
1767		acc	ata	aat	αta		cat	ctt	cgg	maa		act	aa+	ata	ata		1444
1768									Arq								1444
1769	m 9	1111	110	ASII	465	Arg	1113	Lieu	AL 9	470	TTG	1111	оту	vai	475	ser	
1771	a.a.a	a 2 a	00+	~+~		+++	~~~										3.400
1772	Cag	gay	Done	y Ly	LLG	D	31-	acc	acg Thr	ala	get	gaa	aac	att	ege	tat	1492
1773	GIII	GIU	P10	480	Leu	Pne	Ald	THE		116	Ата	GIU	Asn		Arg	Tyr	
1775									485					490			
1776									gag								1540
	GIY	Arg		ASI	vai	Thr	met		Glu	TTE	GLu	ьуs		Val	Lys	Glu	
1777			495					500					505				
1779									aaa								1588
1780	Ala		Ala	Tyr	Asp	Phe		Met	Lys	Leu	Pro		Lys	Phe	Asp	${ t Thr}$	
1781		510					515					520					
1783	ctg	gtt	gga	gag	aga	ggg	gcc	cag	ctg	agt	ggt	gga	cag	aaa	cag	aga	1636
1784		Val	Gly	Glu	Arg		Ala	Gln	Leu	Ser		Gly	Gln	Lys	Gln	Arg	
1785	525					530					535					540	
1787									cgc								1684
1788	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Val	Arg	Asn	Pro	Lys	Ile	Leu	Leu	Leu	
1789					545					550					555		
1791	gat	gag	gca	acg	tca	gct	ctg	gac	act	gaa	agt	gaa	gca	gtg	gtt	cag	1732
1792	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Thr	Glu	Ser	Glu	Ala	Val	Val	Gln	
1793				560					565					570			
1795	gtg	gcc	ctg	gat	aag	gcc	aga	aaa	ggc	cgg	act	acc	att	gtg	ata	gct	1780
1796									Gly								
1797			575				-	580	_	-			585				
1799	cat	cgt	ttg	tct	aca	gtt	cqt	aat	gcc	gat	atc	att	act	aat	ttt	gat	1828
1800	His	Arg	Leu	Ser	Thr	Val	Arq	Asn	Ãla	Ãsp	Val	Ile	Ala	Glv	Phe	Asp	
1801		590					595					600		2			
1803	gat	qqa	atc	att	ata	gag	aaa	ασa	aat	cat	gat	gaa	ctc	ata	aaa	σασ	1876
1804									Asn								20,0
1805	605					610		1			615				-10	620	
1807		aac	att	tac	ttc		ctt	atc	aca	atσ		aca	aga	ana	aat		1924
1808	Lvs	Glv	Tle	Tyr	Phe	Lve	Leu	Val	Thr	Met	Glr	Thr	Arc	Cly	Acr	Glu	1724
1809		1		-1-	625	-10				630	3111	* * * * * *	-114 9	GIY	635	GLU	
1811	att	αaσ	tta	паа		acc	act	aat	gaa		222	ant	m = 2	20+		000	1972
1812	Tle	Glu	Leu	Glu	Acr	Δla	Thr	G1.	Glu	Car	Tuc	Cor	Clu	Cor	yaı	31a	13/2
1813		Jiu		640	11011	r L L L	1111	GTĀ	645	Jer	пÃр	261	GIU		ASP	мта	
-013				0.40					043					650			

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1815										tcc							2020
1816	Leu	Glu		Ser	Pro	Lys	Asp		Gly	Ser	Ser	Leu		Lys	Arg	Arg	
1817			655		~ ~ 4			660					665				2068
1819 1820										caa Gln							2008
1821	ser	670	Arg	Arg	ser	тте	675	Ала	PIO	GIII	GIY	680	ASP	Arg	пуѕ	ren	
1823	aat		222	nan	gac	tta		nan	aat	qta	cct		att	tcc	ttc	taa	2116
1824						-		-		Val			_				2110
1825	685	1111	цyз	Oru	r.sp	690	A3II	GIU	ASII	Vul	695	110	vai	DCI	1 110	700	
1827		att	cta	aaσ	cta		tca	act	σаа	tgg		t.at.	ttt	a t.a	att		2164
1828										Trp							
1829	3			•	705					710		-			715	•	
1831	ata	ttt	tgt	gct	att	ata	aac	gga	ggc	ctg	caa	cca	gca	ttt	tca	ata	2212
1832	Ile	Phe	Cys	Āla	Ile	Ile	Asn	Gly	Gly	Leu	Gln	Pro	Ala	Phe	Ser	Ile	
1833				720					725					730			
1835										acc							2260
1836	Ile	Phe	Ser	Arg	Ile	Ile	Gly	Ile	Phe	Thr	Arg	Asp	Glu	Asp	Pro	Glu	
1837			735					740					745				
1839										tct							2308
1840	Thr	-	Arg	Gln	Asn	Ser		Met	Phe	Ser	Val		Phe	Leu	Val	Leu	
1841		750					755					760					2256
1843										ctc	_						2356
1844	_	TTE	тте	ser	Pne	770	Thr	Pne	Pne	Leu	775	GTĀ	Pne	Thr	Pne	780	
1845 1847	765	aa+	~~~	~~~	2+0		201	3 3 0	caa	ctt		+ = 0	a t a	a++	++0		2404
1848										Leu							2404
1849	пуъ	нта	GLY	Giu	785	пец	1111	шуз	Arg	790	AIG	ıyı	ne c	Val	795	AI 9	
1851	tcc	atα	cta	aσa		gat	atc	aαc	taa	ttt	gat	gac	cct	aaa		acc	2452
1852		_	-		-	-	-	-		Phe	_	_					
1853				800					805					810	_		
1855	act	qqa	gca	ttg	aca	acc	agg	ctt	gcc	aat	gat	gçq	gct	caa	gtt	aaa	2500
1856	Thr	Gly	Ăla	Leu	Thr	Thr	Arg	Leu	Āla	Asn	Ásp	Ala	Ála	Gln	Val	Lys	
1857			815					820					825				
1859										att							2548
1860	Gly	Ala	Ile	Gly	Ser	Arg	Leu	Ala	Val	Ile	Thr		Asn	Ile	Ala	Asn	
1861		830					835					840					
1863										atc							2596
1864		Gly	Thr	Gly	Ile		Ile	Ser	Leu	Ile		Gly	Trp	Gin	Leu		
1865	845					850					855					860	2644
1867										att							2644
1868	Leu	Leu	Leu	ьеų	865°		Val	Pro	me	Ile 870	Ald	me	Ald	GIĀ	875	Vdl	
1869 1871	~~~	2+4		2+4			~~~		~~~	ctg	222	~ a +	220	222		ot a	2692
1872										Leu							2032
1873	GIU	rict	пуз	880	ьeu	er.	GTÄ	GTII	885	neu	пyз	vəħ	υχэ	890	GIU	Leu	
1875	gaa	σσε	act		aad	att	act	aca		gcc	atc	gaa	aac		cga	act	2740
1876										Ala							2,10
1877		1	895	1	-, -			900					905				
1879	gtt	gtt		ttq	act	cgq	gag		aag	ttt	gaa	tac	atg	tat	gca	cag	2788
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1880 1881	Val	Val 910	Ser	Leu	Thr	Arg	Glu 915	Gln	Lys	Phe	Glu		Met	Tyr	Ala	Gln	
1883	agt			αta	cca	tan			+ ~ +	***		920				ttc	
1884	Ser	Len	Gln	Va1	Pro	Tur	Ara	Aco	COT	Tou	agg	aaa	gca	cac	atc	ttc	2836
1885	925	цец	GIII	val	FIO	930	мту	ASII	ser	Leu		ьуs	Ala	His	ITe		
1887			+ 00	+++	+ a+		200	~~-			935					940	
1888	999	Val	Con	Dha	tct	TIO	mbr	Cag	gca	atg	atg	tat	ttt	tcc	tat	gct	2884
1889	Gry	Val	361	FILE	Ser 945	116	1111	GIII	Ala		мет	Tyr	Phe	Ser		Ala	
1891	aac	tat	tto	oaa			~~~	+ 2 0	++~	950					955		
1892	612	Cue	Pho	224	ttt Phe	29 L	315	Term	LLG	grg	gca	aat	gag	ttc	atg	aac	2932
1893	OL,	Cys	1110	960	riic	GIY	Ата	тут	965	Val	Ата	Asn	GIU		Met	Asn	
1895	+++	car	mat.		ctt	++~	at a	++0						970			
1896	Phe	Gln	Aen	Val	Leu	Leu	y La	Dho	Con	31-	att	gtc	מטט	ggt	gcc	atg	2980
1897		0111	975	Val	ыси	Бец	Val	980	ser	Ald	TTE	val		GIĀ	Ala	Met	
1899	gca	ata		cad	gtc	ant	tca		aat	aat	~~~	+-+	985				2000
1900	Ala	Val	614	Cln	Val	Sor	Cor	Dha	312	Dwo	yac	Tat	gcc	aaa	gcc	aaa	3028
1901		990	OLY	0111	vul	DCI	995	rne	ніа	PIO		1000	Ата	ràs	Ата	ьys	
1903	αta		aca	acc	cac	atc		atα	2+0	2++		1000				- 4-4	2076
1904	Val	Ser	Ala	Ala	His	Val	Tle	Mo+	Tla	Tlo	Clu	Tua	con	CCL	ctg	att	3076
1905	100	5		1114		1010	1	TIC C	116	116	1015		ser	PIO	Leu		
1907			tac	age	cct			ctc	220	003	201.	, , , , ,	++~	~~~	~~-	1020	2124
1908	Asp	Ser	Tvr	Ser	Pro	His	Glv	Len	Luc	Dro	Acn	mhr	LLY	gaa	gga	aac	3124
1909			-1-		1025		011	ncu		1030	Mali	1111	neu		1035	ASII	
1911	ata	aca	+++		gag	atc	ata	ttc	220	+=+	000	20+			1032		2170
1912	Val	Thr	Phe	Asn	Glu	Val	Val	Phe	Acn	Tur	Dro	Thr	Ara	Dro	gac	atc	3172
1913				1040	0	, ,,,	• 41		1045	1 y 1	FIO	1111		1050	ASP	ire	
1915	ccc	ata			ggg	cta	age			ata	аал	aan	aaa -	030	200	ata	3220
1916	Pro	Val	Leu	Gln	Gly	Len	Ser	Leu	Glu	Val	T.tre	Luc	010	Cln	mhm	CLG	3220
1917			1055		2		200	1060	oru	• • •	2,10		.065	9111	1111	Leu	
1919	qcc	ctc	qta	aat	agc	agt			ааа	ааσ	age	aca	++n	att	cac	oto	3268
1920	Āla	Leu	Val	Gly	Ser	Ser	Glv	Cvs	Glv	Lvs	Ser	Thr	Val	Val	Cln	LOU	,3200
1921	1	L070		-		1	1075	-10	011	-10		080	V 4 1	*41	GIII	пец	
1923	cta	gag	cgc	ttc	tat			tta	act	aat			cta	att	cat	aac	3316
1924	Leu	Glu	Arg	Phe	Tyr	Asp	Pro	Leu	Ala	Glv	Ser	Val	Len	Tle	Asn	Glv	3310
1925	1085	5	-		-	1090	)			1	1095		204	110	1100	1100	
1927	aaa	gag	ata	aag	cac	ctq	aat	qtc	caq	t a a	ctc	сαа	αса	cac	cta	aac	3364
1928	Lys	Glu	Ile	Lys	His	Leu	Asn	Val	Gln	Trp	Leu	Ara	Ala	His	Leu	Glv	3304
1929				_ 1	1105				1	.110		5			1115	017	
1931	atc	gtg	tct	cag	gag	ccc	atc	ctq	ttt	qac	tac	agc	att	acc	asa	aac	3412
1932	Ile	Val	Ser	Gln	Glu	Pro	Ile	Leu	Phe	Asp	Cvs	Ser	Ile	Ala	Glu	Asn	3412
1933			1	120				1	.125		-4-			130	014	11011	
1935	att	gcc	tat	gga	gac	aac	agc	cgq	qtc	qta	tca	cat	gaa	gag	att	atα	3460
1936	Ile	Ala	Tyr	Gly	Asp	Asn	Ser	Arg	Val	Val	Ser	His	Glu	Glu	Ile	Met	9100
1937		1	.135				1	140				1	145				
1939	cag	gca	gcc	aag	gag	gcc	aac	ata	cac	cac	ttc	atc	gag	aca	ctc	cct	3508
1940	Gln	Ala	Ala	Lys	Glu	Ala	Asn	Ile	His	His	Phe	Ile	Ğlu	Thr	Leu	Pro	5500
1941	1	150				1	155				1	160					
1943	gag	aaa	tac	aac	acc	aga	gta	gga	gac	aaa	gga	acc	caq	ctc	tct	ggt	3556
1944	Glu	Lys	$\mathtt{Tyr}$	Asn	Thr	Arg	Val	Gly	Asp	Lys	Gly	Thr	Gln	Leu	Ser	ĞÎy	

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Input Set : A:\485402\_1.txt
Output Set: N:\CRF3\10062000\1672725.raw

1945 1165 ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa Ala Gly Ala Lys Arg tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac no end of line numbering. See p. 6 tatgtagaac tacctgttia acatttcttg ctgcaactga agatcattcc accaagttca 1977 gagtetteag attttataat taaaggaace aaaagaaaca ttatetgatg gaataaaata ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt 1980 ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat E--> 1981 caaaaaaaa aaaaaaaaaa 2152 <210> SEQ ID NO: 24 2153 <211> LENGTH: 4279 2154 <212> TYPE: DNA 2155 <213> ORGANISM: Canis familiaris 2157 <220> FEATURE: 2158 <221> NAME/KEY: CDS 2159 <222> LOCATION: (17)...(3859) 2161 <400> SEQUENCE: 24 ggagcgcgag gtcggg atg gat cct gaa gga ggc cgt aag ggg agt gca gag Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa gag aag aag Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn 2174 tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile

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2178															atg		244
2179 2180	His	Gly	Ala	Ala	Leu 65	Pro	Leu	Met	Met	Leu 70	Val	Phe	GIĀ	Asn	Met 75	Thr	
2182	ant.	200	+++	002		aca	aaa	a++	t ca		220	222	act	+++	cca	att	292
2183															Pro		2,72
2183	ASP	ser	FIIC	80	ASII	ALG	GIY	116	85	Arg	ASII	пуз	TILL	90	FIO	Var	
						~++							++~			a > +	340
2186															aac		340
2187	TTE	TTE		GIU	ser	TTE	Tnr		Asn	Thr	GIn	HIS		TTE	Asn	HIS	
2188			95					100					105				
2190															atc		388
2191	Leu		Glu	Glu	Met	Thr		Tyr	Ala	Tyr	$\mathtt{Tyr}$		Ser	Gly	Ile	GIY	
2192		110					115					120					
2194															tgc		436
2195	Ala	Gly	Val	Leu	Val	Ala	Ala	Tyr	Ile	Gln	Val	Ser	Phe	Trp	Cys	Leu	
2196	125					130					135					140	
2198	gca	gca	gga	aga	cag	ata	ctc	aaa	att	aga	aaa	caa	ttt	ttt	cat	gct	484
2199	Ala	Ala	Gly	Arg	Gln	Ile	Leu	Lys	Ile	Arg	Lys	Gln	Phe	Phe	His	Ala	
2200					145					150					155		
2202	atc	atq	cga	cag	gag	att	ggc	tgg	ttt	gac	gtg	cat	gac	gtt	ggg	gag	532
2203	Ile	Met	Arg	Gln	Glu	Ile	Gly	Trp	Phe	Asp	Val	His	Asp	Va1	Gly	Glu	
2204				160			_	-	165	-			~	170	-		
2206	ctt	aac	acc	caa	ctc	aca	gac	gat	atc	tcc	aaa	atc	aat	gaa	qqa	att	580
2207															Gly		
2208	200		175		200			180			-10		185	V-u	0-1		
2210	aac	gac		att	ana	atσ	ttc		caa	tca	ata	gca		+++	ttc	acc	628
2211		_				-						-			Phe		020
2212	G <sub>1</sub>	190	цуз	110	Gry	IIC C	195	1 110	OIII	DCI	110	200	1111	1 110	1		
2214	aat		ata	ata	aaa	+++		cat	aat	taa	nss		200	ctt	gtg	att	676
2214															Val		070
2216	205	FIIE	116	Val	GTA	210	1111	Arg	Gry	11P	215	neu	1111	пец	Val	220	
					~~+			~~~	-++	+		~~~	2+4	+~~	~~~		724
2218															gca		/ 24
2219	теп	Ald	ire	ser		val	Leu	GIĀ	Leu		Ald	Ald	тте	ттр	Ala	гуз	
2220					225					230					235		770
2222							-		~			-		_	aaa	_	772
2223	He	Leu	Ser		Phe	Thr	Asp	Lys		Leu	Leu	Ala	Tyr		Lys	Ala	
2224				240					245					250			
2226															att		820
2227	Gly	Ala		Ala	Glu	Glu	Val		Ala	Ala	Ile	Arg		Val	Ile	Ala	
2228			255					260					265				
2230															tta		868
2231	Phe	Gly	Gly	Gln	Lys	Lys	Glu	Leu	Glu	Arg	Tyr	Asn	Lys	Asn	Leu	Glu	
2232		270					275					280					
2234	gaa	gct	aaa	gga	att	ggg	ata	aag	aaa	gct	atc	acg	gcc	aac	att	tct	916
2235	Glu	Ala	Lys	Gly	Ile	Gly	Ile	Lys	Lys	Ala	Ile	Thr	Ala	Asn	Ile	Ser	
2236	285		-	-		290		-	-		295					300	
2238	att	ggt	gcc	gct	ttc	tta	ttg	atc	tat	gca	tca	tat	gct	ctg	gct	ttc	964
2239															Ãla		
2240		-			305				-	310		1			315		
2242	taa	tat	qaa	acc		tta	qtc	ctc	tcc		qaa	tat	tct	att	gga	caa	1012

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2243 2244	Trp	Tyr	Gly	Thr	Ser	Leu	Val	Leu	Ser 325	Ser	Glu	Tyr	Ser	Ile 330	Gly	Gln	•
2246	ata	dta	20+		++0	+++	· + a+	at a	tta	2++	~~~	aat	+++		-++	~~~	1060
2247																	1000
	val	Leu		vai	Pne	Pne	ser		Leu	ire	GTĀ	Ala		ser	116	GIY	
2248			335					340					345				
2250									ttt								1108
2251	Gln	Ala	Ser	Pro	Ser	Ile	Glu	Ala	Phe	Ala	Asn	Ala	Arg	Gly	Ala	Ala	
2252		350					355					360					
2254	tat	gaa	atc	ttc	aaq	ata	att	gac	aat	aaa	cca	age	att	gac	age	tat	1156
2255	Tvr	Ğlu	Ile	Phe	Lvs	Ile	Ile	Asp	Asn	Lvs	Pro	Ser	Ile	Āsp	Ser	Tvr	
2256	365					370					375					380	
2258		aaa	ant	aaa	cat		cca	ma t	aat	2++		aaa	22+	++0	722		1204
2259									Asn								1204
	Set	nys	ser	GLY		пÃР	PIO	wab	ASII		пуѕ	GIY	ASII	ьeu		Pile	
2260					385					390					395		
2262									tct								1252
2263	Lys	Asn	Val		Phe	Ser	Tyr	Pro	Ser	Arg	Lys	Glu	Val	-	Ile	Leu	
2264				400					405					410			
2266	aag	ggt	ctc	aac	ctg	aag	gtt	cag	agt	ggg	cag	aca	gtg	gcg	ctg	gtt	1300
2267	Lys	Gly	Leu	Asn	Leu	Lys	Val	Gln	Ser	Gly	Gln	Thr	Val	Ala	Leu	Val	
2268	_	-	415			_		420					425				
2270	aaa	aac	agt	aac	tac	aaa	ааσ	age	acq	acc	ata	сап	cta	atα	caq	agg	1348
2271									Thr								1340
2272	017	430	DCI	Ory	Cys	Gry	435	DCI	1111	1111	val	440	Leu	Hec	GIII	ALG	
2274																	7.206
									gtc								1396
2275		Tyr	Asp	Pro	Thr		GTĀ	мет	Val	Cys		Asp	GTĀ	GIn	Asp		
2276	445					450					455					460	
2278									cgg								1444
2279	Arg	Thr	Ile	Asn	Val	Arg	His	Leu	Arg	Glu	Ile	Thr	Gly	Val	Val	Ser	
2280					465					470					475		
2282	caq	gag	cct	gtg	ttq	ttt	gcc	acc	acq	ata	act	qaa	aac	att	cac	tat	1492
2283									Thr								
2284				480					485					490	5	-1-	
2286	aac	cac	gaa		atc	acc	a±α	cat	gag	att	mam	222	act		220	ma a	1540
2287		-	•		-		_	-	Glu				_	_	_	-	1340
2288	GIY	AI 9	495	ASII	Val	1111	Mec	500	GIU	116	GIU	цуз	505	Val	пÃЭ	GIU	
2290	~~~	a a +		+-+	~~+	+++	.+.			a+ a	~~+						1500
									aaa								1588
2291	ALA		АТА	Tyr	Asp	Pne		met	Lys	Leu	Pro		Lys	Phe	Asp	Thr	
2292		510					515					520					
2294									ctg								1636
2295	Leu	Val	Gly	Glu	Arg	Gly	Ala	Gln	.Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	
2296	525					530					535					540	
2298	atc	qcc	att	qct	cqq	qcc	cta	qtt	cqc	aac	ccc	aaq	att	ctt	cta	cta	1684
2299									Arg								
2300	_	_	_	_	545	_				550		-2-5			555		
2302	nat	gag	aca	acc		act	ctc	a a c	act		ant	ma.	ac.	ata		030	1732
2302									Thr								1132
	ASP	GIU	WIG		ser	HIG	ьeu	ASD		GIU	ser	GIU	WTG		val	GTII	
2304				560					565					570			1.000
2306									ggc								1780
2307	Val	Ala	Leu	Asp	Lys	Ala	Arg	Lys	Gly	Arg	Thr	Thr	Ile	Val	Ile	Ala	

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2308			575					580					585				
2310	cat	aat		tat	aca	a++	aat		acc	ara t	at a	a++		~~+	+++	ast	1828
2310					Thr												1020
2311	ura	590	Leu	ser	1111	val	595	ASII	Ala	ASP	val	600	AId	GIĀ	Pne	ASP	
										4-							1076
2314					gtg												1876
2315		GIA	vaı	тте	Val		rys	GIĀ	Asn	HIS		GIu	Leu	Met	гăг		
2316	605					610					615					620	
2318					ttc												1924
2319	Lys	Gly	Ile	${ t Tyr}$	Phe	Lys	Leu	Val	Thr		Gln	Thr	Arg	Gly	Asn	Glu	
2320					625					630					635		
2322					aat												1972
2323	Ile	Glu	Leu	Glu	Asn	Ala	Thr	Gly	Glu	Ser	Lys	Ser	Glu	Ser	Asp	Ala	
2324				640					645					650			
2326	ttg	gaa	atg	tct	cca	aaa	gat	tca	ggg	tcc	agt	tta	ata	aaa	aga	aga	2020
2327	Leu	Glu	Met	Ser	Pro	Lys	Asp	Ser	Gly	Ser	Ser	Leu	Ile	Lys	Arg	Arg	
2328			655					660					665				
2330	tca	act	cqc	agg	agt	ata	cat	gca	cca	caa	qqc	caa	gac	aga	aaq	ctt	2068
2331					Ser												
2332		670	_	-			675				^	680	•	_	-		
2334	aat.	aca	aaa	gag	gac	tta	aat	gag	aat	qta	cct	cca	att	tcc	ttc	t.aa	2116
2335					Asp												
2336	685		-1-			690					695					700	
2338		att	cta	ааσ	ctg		tca	act	gaa	tαα		tat	+++	ata	att		2164
2339					Leu												2201
2340	1119	110		_, _	705	21311	JCI	1111	OIU	710	110	- 7 -		, a _	715	GII	
2342	a + a	+++	+ a+	aat	att	a+ a	220	aa 3	aaa		~ ~ ~	003	aa.	+++		a+ a	2212
2342					Ile												2212
2343	TTE	FIIE	Cys	720	TTE	TTE	ASII	GIY	725	Leu	GIII	PIO	MIG	730	ser	He	
2344	2+2	+++	+ ~ ~		~++	2+2	~~~	2+0		200		+	~~~		aat	~~~	2260
2347					att												2200
2347	116	Pne	735	Arg	Ile	116	GIĀ	740	PHE	THE	Arg	ASP	745	ASD	PIO	GIU	
2340				~~~		~~+					~+ ~						2200
					aat												2308
2351	Thr	-	Arg	GII	Asn	ser		мет	Phe	ser	Val		Pne	Leu	Val	Leu	
2352		750	٠				755					760					0055
2354					ttt												2356
2355		шe	iie	ser	Phe		Thr	Pne	Pne	Leu		GTĀ	Pne	Thr	Phe		
2356	765					770					775					780	
2358					atc												2404
2359	Lys	Ala	GLY	Glu	Ile	Leu	Thr	Lys	Arg		Arg	$\mathbf{T}\mathbf{y}\mathbf{r}$	Met	Val		Arg .	
2360					785					790					795		
2362					cag												2452
2363	Ser	Met	Leu		Gln	Asp	Val	Ser	-	Phe	Asp	Asp	Pro	-	Asn	Thr	
2364				800					805					810			
2366					aca												2500
2367	Thr	Gly	Ala	Leu	Thr	Thr	Arg	Leu	Ala	Asn	Asp	Ala	Ala	Gln	Val	Lys	
2368			815					820					825				
2370					tcc												2548
2371	Gly	Ala	Ile	Gly	Ser	Arg	Leu	Ala	Val	Ile	Thr	Gln	Asn	Ile	Ala	Asn	
2372		830					835					840					

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2374	ctt	ggg	aca	ggc	att	att	ata	tcc	tta	atc	tat	ggt	tgg	caa	tta	aca	2596
2375 2376	Leu 845	GIy	Thr	Gly	Ile	Ile	Ile	Ser	Leu	Ile			${\tt Trp}$	Gln	Leu		
2378						850					855					860	
2379	LOU	LLa	Tou	ta	gca	att	gta	ccc	atc	att	gca	ata	gca	gga	gtt	gtt	2644
2380	Leu	пеи	теп	Leu	Ala 865		yaı	Pro	ııe		Ala	He	Ala	Gly		Val	
2382	~ ~ ~	a t a	227	¬+~						870					875		
2383	Glu	Met	Luc	Mot	ttg Leu	Cor	gga	Cla	gca	CLG	aaa	gat	aag	aaa	gag	cta	2692
2384	GIU	nec	шуз	880	пец	361	GIY	GIII	885	Leu	гĀЗ	Asp	гăг		GLu	Leu	
2386	даа	ада	act		aag	att	act	202		aaa	240	~~~	226	890			2740
2387	Glu	Glv	Ala	Glv	Lys	Tle	Δla	Thr	Glu	λla	Tlo	Clu	aac Aan	Dho	cya	act mb	2740
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2390	att	att		tta	act	caa	gag			+++	ra a	tac		tat	aca	a2a	2788
2391	val	Val	Ser	Leu	Thr	Arq	Glu	Gln	Lvs	Phe	Glu	Tvr	Met	Tur	Δla	Gln	2700
2392		910			•		915		-1-	• •••		920	1100	~1-	111.0	0111	
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2395	Ser	Leu	Gln	Va1	Pro	Tyr	Arg	Asn	Ser	Leu	Arq	Lvs	Ala	His	Ile	Phe	2000
2396	925					930					935					940	
2398	ggg	gtc	tca	ttt	tct	atc	acc	cag	gca	atg	atg	tat	ttt	tcc	tat	gct	2884
2399	Gly	Val	Ser	Phe	Ser	Ile	Thr	Gln	Ala	Met	Met	Tyr	Phe	Ser	Tyr	Ala	
2400					945					950					955		
2402	ggc	tgt	ttc	cgg	ttt	ggt	gcc	tac	ttg	gtg	gca	aat	gag	ttc	atg	aac	2932
2403	Gly	Cys	Phe	Arg	Phe	Gly	Ala	Tyr	Leu	Val	Ala	Asn	Glu	Phe	Met	Asn	
2404				960					965					970			
2406	ttt	cag	gat	gtt	ctt	ttg	gta	ttc	tca	gct	att	gtc	ttt	ggt	gcc	atg	2980
2407	Pne	GIn	Asp	Val	Leu	Leu	Val		Ser	Ala	Ile	Val		Gly	Ala	Met	
2408 2410			975					980					985				
2410	y Ca	gra	999	cag	gtc	agt	tca	ttt	gct	cct	gac	tat	gcc	aaa	gcc	aaa	3028
2411	Ата	990	GTÀ	GIII	Val	ser		Pne	Ala	Pro			Ala	Lys	Ala	Lys	
2414	at a		~~ a	acc	a 2 a	ata	995	~ + ~	- 4			L000					
2415	Val	Sar	Δla	Δla	cac His	3751	Tio	Mot	atc	att	gaa	aaa	agc	cct	ctg	att	3076
2416	1009	5001	AIG	ALG	птэ	1010	, 116	Met	116	тте	1015		ser	Pro	Leu		
2418			tac	age	cct			ctc	220	003			++~	~		1020	2104
2419	Asp	Ser	Tvr	Ser	Pro	His	Glv	Ten	Lve	Pro	aa L Aen	Thr	LLY	Clu	99a	Aar	3124
2420			-1-	1	1025		011	<b></b> cu		1030	ASII	1111	Deu		1035	ASII	
2422	qtq	aca	ttt		gag	atc	ata	t.t.c			ccc	act	caa			ato	3172
2423	Val	Thr	Phe	Asn	Glu	Val	Val	Phe	Asn	Tvr	Pro	Thr	Ara	Pro	Asp	Tle	31/2
2424			1	040					L045	-1-				050	пор	110	
2426	ccc	gtg	ctc	cag	ggg	ctg	agc	ctc	gag	ata	aaq	aaq			acα	cta	3220
2427	Pro	Val	Leu	Gln	Gly	Leu	Ser	Leu	Ğlü	Val	Lys	Lvs	Glv	Gln	Thr	Leu	0220
2428		1	.055				1	.060				1	065				
2430	gcc	ctc	gta	ggt	agc	agt	ggc	tgt	ggg	aag	agc	aça	gtt	gtt	caq	ctc	3268
2431	Ala	Leu	Val	Gly	Ser	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Val	Val	Gln	Leu	
2432	1	.070				1	.075				1	080					
2434	cta	gag	cgc	ttc	tat	gac	ccc	ttg	gct	ggt	tca	gtg	cta	att	gat	ggc	3316
2435	Leu	Glu	Arg	Phe	Tyr	Asp	Pro	Leu	Ala	Gly	Ser	Val	Leu	Ile	Asp	Gly	
2436	1085					1090					1095				_	1100	
2438	aaa	gag	ata	aag	cac	ctg	aat	gtc	cag	tgg	ctc	cga	gca	cac	ctg	ggc	3364

RAW SEQUENCE LISTING DATE: 10/06/2000 PATENT APPLICATION: US/09/672,725 TIME: 12:46:04 Input Set : A:\485402\_1.txt Output Set: N:\CRF3\10062000\I672725.raw 2439 Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly 2442 atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac 2443 Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att atg Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly 1165 1170 1180 ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct
Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
1185 1190 1195 cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc Glu Lys Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
1265 1270 1275 gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tatttttaa Ala Gly Ala Lys Arg tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accaagttca gagtetteag attttataat taaaggaace aaaagaaaea ttatetgatg gaataaaata 2489 ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat E--> 2492 caaaaaaaa aaaaaaaaa 2663 <210> SEQ ID NO: 26 ) refer to p.6 2664 <211> LENGTH: 4279 2665 <212> TYPE: DNA 2666 <213> ORGANISM: Canis familiaris 2668 <220> FEATURE: 2669 <221> NAME/KEY: CDS

2670 <222> LOCATION: (17)...(3859)

DATE: 10/06/2000 TIME: 12:46:05

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2674				-	, , , ,	let A	sp F	ro (	2111 6	110 6	1111 7	vac t	iag ç	13	igt s	Ala G	19	52
2675						1		(	, Lu	5	эту г	119 1	ıys c	TA 5	10	AIA G.	Lu	
2677	aaq	r aac	tto	: tac	r aaa		aac								Τ0	g aaa		
2678	Lvs	Asr	Phe	Trn	Tive	Met	G1v	7 T.376	. Luc	cor	- aac	aaa	i dad	gag	aaq	g aaa E Lys		100
2679			15			, 1100	. Gry	20	, па	261	. гус	з гъ			і гуз	Lys		
2681	gaa	aad			act	ato	200						25	, .		aat		
2682	Glu	Litvs	Lve	Pro	Thr	. Val	Car	mb.	Dha	. 90a	atg	ו ככנ	. cgc	: tat	tea	aat Asn		148
2683		30				Val	35	1111	Pne	. Ald	і мет			туг	· Sei	Asn		
2685	taa			agg	++0	+ + + +						40						
2686	Trn	T.AII	) Jan	720	Tou	m-r-	Mot	1 1 1 2	9 69	999	aca	arg	gct	gec	ato	atc		196
2687	45	Leu	. Mop	, ara	пец	. 1y1 50	nec	. ren	val	GIA			Ala	Ala	Il∈	Ile		
2689			aat	~~~	a+ a						5.5	•				60		
2690	Hic	Clu	y 0 ι λ 1 ъ	y Ca	Tou	Dec	Ctc	atg	atg	ctg	gtt	ttt	gga	aac	atg	aca		244
2691	1113	GIY	мта	міа	65	PIO	Leu	met	Met	Leu	Val	Phe	Gly	Asn	Met	Thr		
2693	ant.	200	+++	~~~						70					75	,		
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2695	ASP	ser	Phe	Ald	ASI	Ala	GTA	ile	Ser	Arg	Asn	Lys	Thr	Phe	Pro	Val		
2697	.+.			80					85					90				
2698	Tla	a L L	aat	gaa	agt	att	acg	aac	aat	aca	caa	cat	ttc	atc	aac	cat		340
2699	116	тте	ASI	GIU	ser	шe	Thr	Asn	Asn	Thr	Gln	His	Phe	Ile	Asn	His		
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2707	123					T30					135					140		
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2710	Ala	Ala	Gly	Arg	Gin	Ile	Leu	Lys	Ile	Arg	Lys	Gln	Phe	Phe	His	Ála		
2711					145					150					155			
2713	atc	atg	cga	cag	gag	att	ggc	tgg	ttt	gac	gtg	cat	gac	qtt	qqq	gag		532
2714	He	Met	Arg	GIn	Glu	Ile	Gly	Trp	Phe	Asp	Val	His	Asp	Val	Glv	Glu		
2715				T P O					165					170				
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2718	Leu	Asn	Thr	Arg	Leu	Thr	Asp	Asp	Val	Ser	Lys	Ile	Asn	Ğlu	Ğĺv	Ile		
2719			T/5					180					185		_			
2721	ggc	gac	aaa	att	gga	atg	ttc	ttt	caa	tca	ata	qca	aca	ttt	ttc	acc		628
2722	Gly	Asp	Lys	Ile	Gly	Met	Phe	Phe	Gln	Ser	Ile	Ála	Thr	Phe	Phe	Thr		020
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2/30	Leu	Ala	Ile	Ser	Pro	Val	Leu	Glv	Leu	Ser	Ala	Ala	Tla	Trn	λla	Lug		124
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2743		270					275			_	-	280					
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2746	Glu	Ala	Lys	Gly	Ile	Gly	Ile	Lys	Lys	Āla	Ile	Thr	Ãla	Asn	Ile	Ser	
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2771	261	пуs	361	GTÀ	385	гуу	PIO	ASP	Asn		rās	GIŸ	Asn	Leu		Phe	
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2779	4 -	2	415			-, -		420	DCI	CLy	GIII	1111	425	мта	ьеи	Val	
2781	aaa	aac		ggc	t.ac	aaa	aaσ		acg	acc	ata	саσ		ato	020	300	1348
2782	Gly	Asn	Ser	ĞÎv	Cvs	Glv	Lvs	Ser	Thr	Thr	Val	Gln	Len	Mot	Cln	Ara	1340
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2794	Gln	Glu	Pro	Val	Leu	Phe	Ala	Thr	Thr	Ile	Ala	Ğlu	Asn	Ile	Arq	Tvr	
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2830	Lys	Gly	Ile	Tyr	Phe	Lys	Leu	Val	Thr	Met	Gln	Thr	Arg	Gly	Asn	Ğlu		
2831					625					630			_	_	635			
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2835				640		•			645					650	_			
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2838	Leu	Glu	Met	Ser	Pro	Lys	Asp	Ser	Gly	Ser	Ser	Leu	Ile	Lys	Arg	Arg		
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2843		670					675					680						
2845		aça																2116
2846		Thr	Lys	Glu	Asp	Leu	Asn	Glu	Asn	Val	Pro	Pro	Val	Ser	Phe	Trp		
2847	685					690					695					700		
2849		att																2164
2850	Arg	Ile	Leu	Lys		Asn	ser	Thr	Glu		Pro	Tyr	Phe	Val	Val	Gly		
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2871					785					790					795		
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2902					Thr												_,
2903		910					915		-1-			920		-1-			
2905	a'g t	tta	caa	qta	cca	tac		aac	tct	ttσ	aσσ	aaa	qca	cac	atc	ttc	2836
2906	_	-			Pro		_			-			-				
2907	925					930					935					940	
2909	aaa	atc	tca	ttt	tct	atc	acc	caq	qca	atq	atq	tat	ttt	tcc	tat	act.	2884
2910					Ser												
2911	-			,	945					950		-			955		
2913	qqc	tqt	ttc	cqq	ttt	aat	qcc	tac	tta	ata	qca	aat	qaq	ttc	atq	aac	2932
2914					Phe												
2915	-	-		960		-		-	965					970			
2917	ttt	cag	gat	qtt	ctt	ttq	qta	ttc	tca	qct	att	qtc	ttt	ggt	qcc	atq	2980
2918					Leu												
2919			975					980					985				
2921	qca	ata	aaa	cag	gtc	agt.	tca	ttt	act	cct	gac	tat	acc	aaa	acc	aaa	3028
2922					Val												
2923	-	990	2				995				-	1000		-1-		2	
2925	qta	,	qca	qcc	cac	atc		ato	atc	att	-		age	cct	cta	att	3076
2926					His												20,0
2927	1005					1010					1015			0		1020	
2929			tac	age	cct			ctc	aaσ	сса			tta	gaa	σσα		3124
2930	-	-		-	Pro				-			-	_	_			
2931			. 4 -		1025				-	L030					L035		
				_	1				_					-			

RAW SEQUENCE LISTING RAW SEQUENCE LISTING DATE: 10/06/2000 PATENT APPLICATION: US/09/672,725 TIME: 12:46:05

2933	gtg ac	a tti	t aat	gag	gto	gtg	tto	aac	: tat	ccc	act	сαа	cca	gac	ato	3172
2934	AGT II	ır Phe	= ASI	I GT	ı Val	Val	Phe	a Asr	Tyr	Pro	Thr	Ara	Pro	Asp	Tle	31/2
2935			1040	,				1045	)				1050			
2937 2938	ccc gt	g cto	cag	3 9 9 9	, ctg	agc	cto	gag	r gtg	raag	, aag	ggc	cag	acq	cta	3220
	Pro Va	t nec	1 GTI	ı Gly	, Leu	Ser	ьеι	ı Glu	\Val	Lys	Lys	Gly	Gln	Thr	Leu	3220
2939		700	,				1060	)				1065				
2941 2942	gcc ct	c gta	ı ggt	ago	agt	ggc	tgt	ggg	aag	ago	aca	gtt	gtt	caq	ctc	3268
2942	*****	u vai	Gly	Ser	Ser	GTĀ	Cys	Gly	Lys	Ser	Thr	Val	Val	Gln	Leu	+200
2943	10/	U				TO/2					1080					
2945	cta ga	g cgc	tto	tat	gac	ccc	ttg	r gct	ggt	tca	gtg	cta	att	gat	qqc	3316
2946	Leu G1 1085	u Arg	Phe	Tyr	. Asp	Pro	Leu	ı Ala	Gly	Ser	Val	Leu	Ile	Asp	Gly	
2947	1000				109	U				109	5				1100	
2949	aaa ga	g ata	aag	cac	ctg	aat	gtc	cag	tgg	ctc	cga	gca	cac	ctg	ggc	3364
2951	Lys Gl	n ite	: гуз	HIS	Leu	Asn	Val	Gln	Trp	Leu	Arg	Ala	His	Leu	Gly	_
2953				TIOD					1110				-	1116		
2954	atc gt	g tet	cag	gag	ccc	atc	ctg	ttt	gac	tgc	agc	att	gcc	gag	aac	3412
2955	Ile Va	T SET	GIH	GIU	Pro	He	Leu	Phe	Asp	Cys	Ser	Ile	Ala	Glu	Asn	
2957			1120					1125				1	130			
2958	att gc	u Lat	gga	gac	aac	agc	cgg	gtc	gta	tca	cat	gaa	gag	att	gtg	3460
2959	Ile Al	1135	GTA	ASP	Asn	Ser	Arg	Val	Val	Ser			Glu	Ile	Val	
2961	can no			~~~	~		L140				1	.145				
2962	Cag gc	ı gcc aλla	Tuc	Clu	315	aac	ata	cac	cac	ttc	atc	gag	aca	ctc	cct	3508
2963	Gln Ala 1150	י הדמ ו	пуs	GIU	Ala	ASN	TTE	His	His	Phe	Ile	Glu	Thr	Leu	Pro	
2965			220	300		1155				-	1160					
2966	gag aaa	Tur	Acn	Thr.	aya Ara	gta Val	gga	gac	aaa	gga	acc	cag	ctc	tct	ggt	3556
2967	Glu Lys 1165	,.	USII	TIII	1170	vaı	GTĀ	Asp	гàг	GIY	Thr	Gln	Leu	Ser		
2969		ı aaa	can	cac	21/C	, ,	2+2	~~+		1175					1180	
2970	ggc cag Gly Glr	Tive	Gln	Ara	Tla	31a	tla	get	cgc	gct	ctt	gtt	aga	cag	cct	3604
2971		. 275	1	185	116	нта	116	Ald	190	Ala	Leu	Val			Pro	
2973	cat att	tta			gat	maa	ac+	302	190	~~+			1	195		
2974	His Ile	Leu	Leu	Len	Asn	Glu	Δla	Thr	Con	31a	ctg	gat	aca	gaa	agt	3652
2975		1	L200		p	<b>514</b>	71 u	1111	ser	AId	ren .			Glu	Ser	
2977	gaa aag	qtt	qtc	caa	αаа	acc	cta	0203	222	~~~	202		210			
2978	Glu Lys	Val	Val	Gln	Glu	Ala	Len	Asn	Luc	Ala	Ara /	gaa	ggc	cgc	acc	3700
2979	_	1215				1	220	LISP	БYЗ	лта		225	ary .	Arg	Thr	
2981	tgc att	gtg	atc	qcc	cac	cac	tta	tcc	acc	atc	cac	 +	~~~	~~+		27.40
2982	Cys Ile	Val	Ile	Āla	His	Ara	Leu	Ser	Thr	Tla	Cln :	aat i	yca i	yat Nam	tta	3748
2983	1230				1	235				1	240					
2985	ata gtg	gtg	ttt	cag	aat	qqc i	aaa	gtc	ааσ	a a a	nat d	700		~~+		2706
2986	Ile Val	Val	Phe	Gln	Asn	Glv	Lvs	Val	Lvs	Glu	Hie (	390 d	Dhr I	dat.	caa ~~	3796
2987	1217				TZ20					1255					1260	
2989	cag ctg	ctg	gcc	cag	aaa (	ggc a	atc	tat	+++	tcc	ata a	rtc :	art r			2044
2990	Gln Leu	Leu	Ala	Gln	Lys (	Gly :	Ile	Tvr	Phe	Ser	Met I	7al o	igu s	751 /	Jay	3844
2991			Τ.	∠o⊃				1	270				1.	775		
2993	gct gga	gca	aag	cgc	tagto	gaact	tg t	qqcc	ata+	a aa	ctatt	222	tatt	:/J	- 2 2	3000
2994	Ala Gly	Ala	Lys	Arg				,,		, ~9		-uuu	LULI		Laa	3899
2995		1	280													
2997	tatttgt	gtt a	aaac	atgg	c att	taat	caa	agti	taaa	agg 1	tgago	acti	a ct	agaa	aaac	3959
								-			, ,,,,			- 22-46		2222

RAW SEQUENCE LISTING

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DATE: 10/06/2000 TIME: 12:46:05

	2998	tatgtagaac	tacctgttta	aca++++++				
	2999	gagtettean	attttatat	acattttttg	ctgcaactga	agatcattcc	accaagttca	4019
	2000	ccygryttaa	ttgcattata	aaattataga	gtaattcaaa	ataaa++++	gaataaaata ttaataaatt	40/9
	3002	ggtaaaaagt	actgaatgtt	tasstassas	CLLacigett	tgctgaaaga	ttaataaatt ttatagaagt acttttatat	4199
E>	3003	Caaaaaaaa	aaaaaaaaa	ryaaraaagt	gctagctata	ataaaactaa	acttttatat	4259
		caaaaaaaaa	ddddaaaaaa					4233

O9/672, 725

Seg # 28 <210> 28

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

nnt tttttt tttttttt tttttttt ttcgccggcg acttaagatc tt

52

> missing mandatory (220) to (223) features to explain "n's" in sequence. Sec. #10 on Error Summary Sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/672,725

DATE: 10/06/2000 TIME: 12:46:06

Input Set : A:\485402\_1.txt

Output Set: N:\CRF3\10062000\1672725.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No L:15 M:270 C: Current Application Number differs, Replaced Current Application No L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:362 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2 L:499 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2 L:874 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:4317 SEQ:3 L:1981 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2 L:1981 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:22 L:2492 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2 L:2492 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:22 L:3003 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2 L:3003 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2 L:3003 M:352 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:24 L:3183 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28 L:3183 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28 L:3183 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28